

RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/10/028,392

TIME: 08:00:13

Input Set : A:\ES.txt

Output Set: N:\CRF3\01152002\J028392.raw

ENTERED

3 <110> APPLICANT: Bristol-Myers Squibb Company

5 <120> TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN

EXPRESSED

6 PREDOMINATELY IN NERVOUS SYSTEM TISSUES, HLRRNS1

8 <130> FILE REFERENCE: D0085.np

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/028,392

C--> 10 <141> CURRENT FILING DATE: 2001-12-20

10 <150> PRIOR APPLICATION NUMBER: US 60/259,479

11 <151> PRIOR FILING DATE: 2001-01-03

13 <150> PRIOR APPLICATION NUMBER: US 60/260,616

14 <151> PRIOR FILING DATE: 2001-01-09

16 <160> NUMBER OF SEQ ID NOS: 63

18 <170> SOFTWARE: PatentIn version 3.0

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 2450

22 <212> TYPE: DNA

23 <213> ORGANISM: homo sapiens

25 <220> FEATURE:

26 <221> NAME/KEY: CDS

27 <222> LOCATION: (549)..(2450)

29 <400> SEQUENCE: 1

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32 ctggaaggaa ggaagccagg aaagaaagaa ggaaagaaag gaaggcaaga aggaaggcgg      120
34 gcggcgggcg agggcgcggg gccggacggc aggcggggcg gaggcgagga ggcagagcgg      180
36 cccccccagc cccaccgccc cgctgcgga agccccctcc ccaccagga gccggggagg      240
38 ggggagagcg cgagaggctc caggcccggc cgcagccccg ccccccgcg ctccccgcag      300
40 cgggccttgc accccaaatt cctgagcctc attggggggg tctcccccc acgggcccgg      360
42 catgctgccc cccggaagga acccctctcc tcgctcacga tctcgacagg aagccctgga      420
44 gaactgggga ggcagagacc ccggtggcc ggaggcatgt ggaggggggg gcctgggcgc      480
46 agggagaggg ccagcggaa ccaagccacc agggccccca gcgtccacgc ggagcatgaa      540
48 cattgagg atg gcg cgt gcc cgc ggc tcc ccg tgc ccc ccg ctg ccg ccc      590
49      Met Ala Arg Ala Arg Gly Ser Pro Cys Pro Pro Leu Pro Pro
50      1              5              10
52 ggt agg atg tcc tgg ccc cac ggg gca ttg ctc ttc ctc tgg ctc ttc      638
53 Gly Arg Met Ser Trp Pro His Gly Ala Leu Leu Phe Leu Trp Leu Phe
54 15              20              25              30
56 tcc cca ccc ctg ggg gcc ggt gga ggt gga gtg gcc gtg acg tct gcc      686
57 Ser Pro Pro Leu Gly Ala Gly Gly Gly Val Ala Val Thr Ser Ala
58              35              40              45
60 gcc gga ggg ggc tcc ccg ccg gcc acc tcc tgc ccc gtg gcc tgc tcc      734
61 Ala Gly Gly Gly Ser Pro Pro Ala Thr Ser Cys Pro Val Ala Cys Ser
62              50              55              60
64 tgc agc aac cag gcc agc cgg gtg atc tgc aca cgg aga gac ctg gcc      782
65 Cys Ser Asn Gln Ala Ser Arg Val Ile Cys Thr Arg Arg Asp Leu Ala
66              65              70              75
68 gag gtc cca gcc agc atc ccg gtc aac acg cgg tac ctg aac ctg caa      830
69 Glu Val Pro Ala Ser Ile Pro Val Asn Thr Arg Tyr Leu Asn Leu Gln
70      80              85              90

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72	gag aac ggc atc cag gtg atc cgg acg gac acg ttc aag cac ctg cgg	878
73	Glu Asn Gly Ile Gln Val Ile Arg Thr Asp Thr Phe Lys His Leu Arg	
74	95 100 105 110	
76	cac ctg gag att ctg cag ctg agc aag aac ctg gtg cgc aag atc gag	926
77	His Leu Glu Ile Leu Gln Leu Ser Lys Asn Leu Val Arg Lys Ile Glu	
78	115 120 125	
80	gtg ggc gcc ttc aac ggg ctg ccc agc ctc aac acg ctg gag ctt ttt	974
81	Val Gly Ala Phe Asn Gly Leu Pro Ser Leu Asn Thr Leu Glu Leu Phe	
82	130 135 140	
84	gac aac cgg ctg acc acg gtg ccc acg cag gcc ttc gag tac ctg tcc	1022
85	Asp Asn Arg Leu Thr Thr Val Pro Thr Gln Ala Phe Glu Tyr Leu Ser	
86	145 150 155	
88	aag ctg cgg gag ctc tgg ctg cgg aac aac ccc atc gag agc atc ccc	1070
89	Lys Leu Arg Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro	
90	160 165 170	
92	tcc tac gcc ttc aac cgc gtg ccc tcg ctg cgg cgc ctg gac ctg ggc	1118
93	Ser Tyr Ala Phe Asn Arg Val Pro Ser Leu Arg Arg Leu Asp Leu Gly	
94	175 180 185 190	
96	gag ctc aag cgg ctg gaa tac atc tcg gag gcg gcc ttc gag ggg ctg	1166
97	Glu Leu Lys Arg Leu Glu Tyr Ile Ser Glu Ala Ala Phe Glu Gly Leu	
98	195 200 205	
100	gtc aac ctg cgc tac ctc aac ctg ggc atg tgc aac ctc aag gac atc	1214
101	Val Asn Leu Arg Tyr Leu Asn Leu Gly Met Cys Asn Leu Lys Asp Ile	
102	210 215 220	
104	ccc aac ctg acg gcc ctg gtg cgc ctg gag gag ctg gag ctg tcg ggc	1262
105	Pro Asn Leu Thr Ala Leu Val Arg Leu Glu Glu Leu Glu Leu Ser Gly	
106	225 230 235	
108	aac cgg ctg gac ctg atc cgc ccg ggc tcc ttc cag ggt ctc acc agc	1310
109	Asn Arg Leu Asp Leu Ile Arg Pro Gly Ser Phe Gln Gly Leu Thr Ser	
110	240 245 250	
112	ctg cgc aag ctg tgg ctc atg cac gcc cag gta gcc acc atc gag cgc	1358
113	Leu Arg Lys Leu Trp Leu Met His Ala Gln Val Ala Thr Ile Glu Arg	
114	255 260 265 270	
116	aac gcc ttc gac gac ctc aag tcg ctg gag gag ctc aac ctg tcc cac	1406
117	Asn Ala Phe Asp Asp Leu Lys Ser Leu Glu Glu Leu Asn Leu Ser His	
118	275 280 285	
120	aac aac ctg atg tcg ctg ccc cac gac ctc ttc acg ccc ctg cac cgc	1454
121	Asn Asn Leu Met Ser Leu Pro His Asp Leu Phe Thr Pro Leu His Arg	
122	290 295 300	
124	ctc gag cgc gtg cac ctc aac cac aac ccc tgg cat tgc aac tgc gac	1502
125	Leu Glu Arg Val His Leu Asn His Asn Pro Trp His Cys Asn Cys Asp	
126	305 310 315	
128	gtg ctc tgg ctg agc tgg tgg ctc aag gag acg gtg ccc agc aac acg	1550
129	Val Leu Trp Leu Ser Trp Trp Leu Lys Glu Thr Val Pro Ser Asn Thr	
130	320 325 330	
132	acg tgc tgc gcc cgc tgt cat gcg ccc gcc ggc ctc aag ggg cgc tac	1598
133	Thr Cys Cys Ala Arg Cys His Ala Pro Ala Gly Leu Lys Gly Arg Tyr	
134	335 340 345 350	
136	att ggg gag ctg gac cag tcg cat ttc acc tgc tat gcg ccc gtc atc	1646

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137	Ile	Gly	Glu	Leu	Asp	Gln	Ser	His	Phe	Thr	Cys	Tyr	Ala	Pro	Val	Ile	
138					355					360					365		
140	gtg	gag	ccg	ccc	acg	gac	ctc	aac	gtc	acc	gag	ggc	atg	gct	gcc	gag	1694
141	Val	Glu	Pro	Pro	Thr	Asp	Leu	Asn	Val	Thr	Glu	Gly	Met	Ala	Ala	Glu	
142				370					375					380			
144	ctc	aaa	tgc	cgc	acg	ggc	acc	tcc	atg	acc	tcc	gtc	aac	tgg	ctg	acg	1742
145	Leu	Lys	Cys	Arg	Thr	Gly	Thr	Ser	Met	Thr	Ser	Val	Asn	Trp	Leu	Thr	
146			385					390					395				
148	ccc	aac	ggc	acc	ctc	atg	acc	cac	ggc	tcc	tac	cgc	gtg	cgc	atc	tcc	1790
149	Pro	Asn	Gly	Thr	Leu	Met	Thr	His	Gly	Ser	Tyr	Arg	Val	Arg	Ile	Ser	
150		400					405					410					
152	gtc	ctg	cat	gac	ggc	acg	ctt	aac	ttc	acc	aac	gtc	acc	gtg	cag	gac	1838
153	Val	Leu	His	Asp	Gly	Thr	Leu	Asn	Phe	Thr	Asn	Val	Thr	Val	Gln	Asp	
154	415				420					425					430		
156	acg	ggc	cag	tac	acg	tgc	atg	gtg	acg	aac	tca	gcc	ggc	aac	acc	acc	1886
157	Thr	Gly	Gln	Tyr	Thr	Cys	Met	Val	Thr	Asn	Ser	Ala	Gly	Asn	Thr	Thr	
158				435					440					445			
160	gcc	tcg	gcc	acg	ctc	aac	gtc	tcg	gcc	gtg	gac	ccc	gtg	gcg	gcc	ggg	1934
161	Ala	Ser	Ala	Thr	Leu	Asn	Val	Ser	Ala	Val	Asp	Pro	Val	Ala	Ala	Gly	
162			450						455				460				
164	ggc	acc	ggc	agc	ggc	ggg	ggc	ggc	cct	ggg	ggc	agt	ggt	ggt	gtt	gga	1982
165	Gly	Thr	Gly	Ser	Gly	Gly	Gly	Gly	Pro	Gly	Gly	Ser	Gly	Gly	Val	Gly	
166		465					470					475					
168	ggg	ggc	agt	ggc	ggc	tac	acc	tac	ttc	acc	acg	gtg	acc	gtg	gag	acc	2030
169	Gly	Gly	Ser	Gly	Gly	Tyr	Thr	Tyr	Phe	Thr	Thr	Val	Thr	Val	Glu	Thr	
170		480				485						490					
172	ctg	gag	acg	cag	ccc	gga	gag	gag	gcc	ctg	cag	ccg	cgg	ggg	acg	gag	2078
173	Leu	Glu	Thr	Gln	Pro	Gly	Glu	Glu	Ala	Leu	Gln	Pro	Arg	Gly	Thr	Glu	
174	495				500					505					510		
176	aag	gaa	ccg	cca	ggg	ccc	acg	aca	gac	ggt	gtc	tgg	ggt	ggg	ggc	cgg	2126
177	Lys	Glu	Pro	Pro	Gly	Pro	Thr	Thr	Asp	Gly	Val	Trp	Gly	Gly	Gly	Arg	
178				515					520					525			
180	cct	ggg	gac	gcg	gcc	ggc	cct	gcc	tcg	tct	tct	acc	acg	gca	ccc	gcc	2174
181	Pro	Gly	Asp	Ala	Ala	Gly	Pro	Ala	Ser	Ser	Ser	Thr	Thr	Ala	Pro	Ala	
182			530						535					540			
184	ccg	cgc	tcc	tcg	cgg	ccc	acg	gag	aag	gcg	ttc	acg	gtg	ccc	atc	acg	2222
185	Pro	Arg	Ser	Ser	Arg	Pro	Thr	Glu	Lys	Ala	Phe	Thr	Val	Pro	Ile	Thr	
186			545					550					555				
188	gat	gtg	acg	gag	aac	gcc	ctc	aag	gac	ctg	gac	gac	gtc	atg	aag	acc	2270
189	Asp	Val	Thr	Glu	Asn	Ala	Leu	Lys	Asp	Leu	Asp	Asp	Val	Met	Lys	Thr	
190		560					565						570				
192	acc	aaa	atc	atc	atc	ggc	tgc	ttc	gtg	gcc	atc	acg	ttc	atg	gcc	gcg	2318
193	Thr	Lys	Ile	Ile	Ile	Gly	Cys	Phe	Val	Ala	Ile	Thr	Phe	Met	Ala	Ala	
194	575				580					585					590		
196	gtg	atg	ctc	gtg	gcc	ttc	tac	aag	ctg	cgc	aag	cag	cac	cag	ctc	cac	2366
197	Val	Met	Leu	Val	Ala	Phe	Tyr	Lys	Leu	Arg	Lys	Gln	His	Gln	Leu	His	
198				595					600					605			
200	aag	cac	cac	ggg	ccc	acg	cgc	acc	gtg	gag	atc	atc	aac	gtg	gag	gac	2414
201	Lys	His	His	Gly	Pro	Thr	Arg	Thr	Val	Glu	Ile	Ile	Asn	Val	Glu	Asp	

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202          610          615          620          2450
204 gag ctg ccc gcc gcc tcg gcc gtg tcc gtg gcc gcc
205 Glu Leu Pro Ala Ala Ser Ala Val Ser Val Ala Ala
206          625          630
209 <210> SEQ ID NO: 2
210 <211> LENGTH: 634
211 <212> TYPE: PRT
212 <213> ORGANISM: homo sapiens
214 <400> SEQUENCE: 2
216 Met Ala Arg Ala Arg Gly Ser Pro Cys Pro Pro Leu Pro Pro Gly Arg
217 1          5          10          15
220 Met Ser Trp Pro His Gly Ala Leu Leu Phe Leu Trp Leu Phe Ser Pro
221          20          25          30
224 Pro Leu Gly Ala Gly Gly Gly Gly Val Ala Val Thr Ser Ala Ala Gly
225          35          40          45
228 Gly Gly Ser Pro Pro Ala Thr Ser Cys Pro Val Ala Cys Ser Cys Ser
229          50          55          60
232 Asn Gln Ala Ser Arg Val Ile Cys Thr Arg Arg Asp Leu Ala Glu Val
233 65          70          75          80
236 Pro Ala Ser Ile Pro Val Asn Thr Arg Tyr Leu Asn Leu Gln Glu Asn
237          85          90          95
240 Gly Ile Gln Val Ile Arg Thr Asp Thr Phe Lys His Leu Arg His Leu
241          100          105          110
244 Glu Ile Leu Gln Leu Ser Lys Asn Leu Val Arg Lys Ile Glu Val Gly
245          115          120          125
248 Ala Phe Asn Gly Leu Pro Ser Leu Asn Thr Leu Glu Leu Phe Asp Asn
249          130          135          140
252 Arg Leu Thr Thr Val Pro Thr Gln Ala Phe Glu Tyr Leu Ser Lys Leu
253 145          150          155          160
256 Arg Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser Tyr
257          165          170          175
260 Ala Phe Asn Arg Val Pro Ser Leu Arg Arg Leu Asp Leu Gly Glu Leu
261          180          185          190
264 Lys Arg Leu Glu Tyr Ile Ser Glu Ala Ala Phe Glu Gly Leu Val Asn
265          195          200          205
268 Leu Arg Tyr Leu Asn Leu Gly Met Cys Asn Leu Lys Asp Ile Pro Asn
269          210          215          220
272 Leu Thr Ala Leu Val Arg Leu Glu Glu Leu Glu Leu Ser Gly Asn Arg
273 225          230          235          240
276 Leu Asp Leu Ile Arg Pro Gly Ser Phe Gln Gly Leu Thr Ser Leu Arg
277          245          250          255
280 Lys Leu Trp Leu Met His Ala Gln Val Ala Thr Ile Glu Arg Asn Ala
281          260          265          270
284 Phe Asp Asp Leu Lys Ser Leu Glu Glu Leu Asn Leu Ser His Asn Asn
285          275          280          285
288 Leu Met Ser Leu Pro His Asp Leu Phe Thr Pro Leu His Arg Leu Glu
289          290          295          300
292 Arg Val His Leu Asn His Asn Pro Trp His Cys Asn Cys Asp Val Leu
293 305          310          315          320

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296 Trp Leu Ser Trp Trp Leu Lys Glu Thr Val Pro Ser Asn Thr Thr Cys
297                               325                               330           335
300 Cys Ala Arg Cys His Ala Pro Ala Gly Leu Lys Gly Arg Tyr Ile Gly
301                               340                               345           350
304 Glu Leu Asp Gln Ser His Phe Thr Cys Tyr Ala Pro Val Ile Val Glu
305                               355                               360           365
308 Pro Pro Thr Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys
309                               370                               375           380
312 Cys Arg Thr Gly Thr Ser Met Thr Ser Val Asn Trp Leu Thr Pro Asn
313 385                               390                               395           400
316 Gly Thr Leu Met Thr His Gly Ser Tyr Arg Val Arg Ile Ser Val Leu
317                               405                               410           415
320 His Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp Thr Gly
321                               420                               425           430
324 Gln Tyr Thr Cys Met Val Thr Asn Ser Ala Gly Asn Thr Thr Ala Ser
325                               435                               440           445
328 Ala Thr Leu Asn Val Ser Ala Val Asp Pro Val Ala Ala Gly Gly Thr
329                               450                               455           460
332 Gly Ser Gly Gly Gly Gly Pro Gly Gly Ser Gly Gly Val Gly Gly Gly
333 465                               470                               475           480
336 Ser Gly Gly Tyr Thr Tyr Phe Thr Thr Val Thr Val Glu Thr Leu Glu
337                               485                               490           495
340 Thr Gln Pro Gly Glu Glu Ala Leu Gln Pro Arg Gly Thr Glu Lys Glu
341                               500                               505           510
344 Pro Pro Gly Pro Thr Thr Asp Gly Val Trp Gly Gly Gly Arg Pro Gly
345                               515                               520           525
348 Asp Ala Ala Gly Pro Ala Ser Ser Ser Thr Thr Ala Pro Ala Pro Arg
349                               530                               535           540
352 Ser Ser Arg Pro Thr Glu Lys Ala Phe Thr Val Pro Ile Thr Asp Val
353 545                               550                               555           560
356 Thr Glu Asn Ala Leu Lys Asp Leu Asp Asp Val Met Lys Thr Thr Lys
357                               565                               570           575
360 Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Phe Met Ala Ala Val Met
361                               580                               585           590
364 Leu Val Ala Phe Tyr Lys Leu Arg Lys Gln His Gln Leu His Lys His
365                               595                               600           605
368 His Gly Pro Thr Arg Thr Val Glu Ile Ile Asn Val Glu Asp Glu Leu
369                               610                               615           620
372 Pro Ala Ala Ser Ala Val Ser Val Ala Ala
373 625                               630
376 <210> SEQ ID NO: 3
377 <211> LENGTH: 640
378 <212> TYPE: PRT
379 <213> ORGANISM: Homo sapiens
381 <400> SEQUENCE: 3
383 Met Leu Asn Lys Met Thr Leu His Pro Gln Gln Ile Met Ile Gly Pro
384 1                               5                               10           15
386 Arg Phe Asn Arg Ala Leu Phe Asp Pro Leu Leu Val Val Leu Leu Ala
387                               20                               25           30

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date